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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                            Database :
                                                                                                                                                       Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             Searched
                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                          seq length: 0
seq length: 2000000000
PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                           195891 seqs, 67900655 residues
                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-331-631A-3_COPY_29_73
252
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                                                                                                                                                                                                                                                                                                                                                                                          SEFDRQEYEECKRQCMQLET.....RCVSQCDKRFEEDIDWSKYD 45
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17.898 Million cell updates/sec
                                                                                                                                                                                                                                                       195891
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	N	_	Result No.	
54	54		54.5	54.5	4.		55	55	55	55	55	57	57	57	57	58	58	59.5	6	64	67	67	67	•	70.5	72	77.5	7.	Score	
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T19225	T02964	S62730	T13049	T32901	T15765	S44822	T02824	ннсн08	T06674	A71601	B55346	WMVZAI	JQ2162	WMVZ94	G71600	T05892	T29699	T28432	JQ1730	T45840	A40558	TSHUP1	T44430	JC5557	S22477	S06398	FWCNAB	S08059	ID	
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45	44	43	42	41	40	39	38	37	36	ა 5	ω 4	ω ω	32	31	30
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20.6	20.8	20.8	20.8	20.8	20.8	20.8	21.0	21.0	21.0	21.0	21.0	21.2	21.2	21.2	21.4
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A41822	TSHUP2	T18593	T18592	в81430	XLHOA	S00219	150255	T28570	B72167	S46854	E69006	T08880	I54209	T15592	F75103
antimicrobial pept	thrombospondin 2 p	hypothetical prote	hypothetical prote	probable prephenat	colipase A precurs	ubiquinolcytochr	108K heat shock pr	hypothetical prote	A29L protein - var	A28L protein - var	glutamate synthase	NMDA receptor-bind	hypothetical prote	hypothetical prote	probable purine NT

## ALIGNMENTS

A,Cross-references: GB.M16891; NID:g167374; PIDN:AAA33071.1; PID A;Experimental source: var. Coker 201
R;Chlan, C.A.; Borroto, K; Kamalay, J.A.; Dure III, L.
Plant Mol. Biol. 9, 533·546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis A;Reference number: S06398
A;Accession: S06911
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-81 <CH2>
C;Comment: This is a seed storage protein. alpha-globulin B precursor (clone C72) - upland cotton N;Alternate names: seed storage protein; vicilin precursor C:Species: Gossyptum hirsutum (upland cotton) C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999 C;Accession: A30838; S06911 R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L. Plant Mol. Biol. 7, 475-489, 1986 A;Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII A; Reference number: A30838
A; Accession: A30838
A; Molecule type: mRNA
A; Residues: 1-588 < CHL> A; Molecule type: DNA A; Residues: 1-509 <CHL> C; Superfamily: glycinin Plant Mol. Biol. 9, 533-546, 1987
A;Title: Developmental biochemistry of cottonseed embryogenesis and germination. XIX. A;Reference number: \$06398
A;Accession: \$08059
A;Status: not compared with conceptual translation alpha-globulin type B precursor (tandem 1) - upland cotton (fragment) N; Alternate names: seed storage protein C:Species: Gossyphum hirsutum (upland cotton) C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 30-Sep-1993 C:Accession: S08059 R:Chlan, C.A.: Borroto, K.; Kamalay, J.A.; Dure III, L. Plant Mol. Biol. 9, 533-546, 1987 DЬ Matches Query Match Best Local 3 QRRYEECQQECRQQE-ERQQPQCQQRCLKRFEQE 5 RQEYEECKRQCMQLETSGQMRRCVSQCDKRFEED 38 30.8%; Similarity 41.2%; Conservative Score 77.5; DB Pred. No. 0.11; 9; Mismatches 35 2; 10; Length 509; Indels PID:9167375 and 1; germination. Gaps 1;

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C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;1-24/Domain: signal sequence #status predicted <
F;25-566/Product: vicilin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. 18, 1173-1176, 1992
Plant Mol. Biol. 18, 1173-1176, 1992
A;Title: Comparison of the structure and nucleotide sequence
A;Reference number: S22477; MUID:92288309
A;Accession: S22477
                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Theobroma cacao (cacao)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: S22477; S22478; S18105; S22050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: glycinin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-605/Product: alpha-globulin type A #status predic
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C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C:Accession: S06398
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C;Keywords: glycoprotein; seed; storage protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-588/Product: alpha-globulin storage proprotein #status predicted <MAT>
F;417/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-452 <MC2>
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A; Residues: 1-566 < MCH>
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A; Accession: S06398
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A; Title: Development
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C; Species: Gossypiu
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                                                                                                                                                                   C; Genetics:
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A; Residues: 1-605 <CHL>
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Conservative
Query Match
Best Local Similarity
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 A; Molecule type: mRNA
A; Residues: 1-1170 <LAW>
                                     A; Reference number: A26155;
A; Accession: A26155
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A; Residues: 1-810 < YAM>
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Matches 14; Conservative
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J. Biol. Chem. 274, 2563-2570, 1999
A;Title: Multiple functional proteins are produced by cleaving Asn-G1
A;Reference number: Z22767; MUID:99107919
A;Accession: 744430
A;Status: 7771-1
C:Species: Homo sapiens (man)
C:Date: 23-Aug-1987 #sequence_revision
C:Accession: A26155 h.34274; A30140; A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein PV100 [imported] - winter squash
C:Species: Cucurbita maxima (winter squash)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: seed C; Comment: This protein is a storage protein which provides nitrogen F; 12-33,16-29/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G. Biosci. Biotechnol. Biochem. 61, 984-988, 1997
A;Title: Primary structure of 6.5k-arginine/glutamate-rich polypeptide A;Reference number: JC5557; MUID:97357433
A;Accession: JC5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arginine/glutamate-rich 6.5K polypeptide - smooth loofah C:Species: Luffa cylindrica (smooth loofah) C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AB019195; NID:g3808061; PIDN:BAA34056.1;
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                                                                                                                                                                                                                                                                      RAEYEVCRLRCQVAERGVEQQRKCEQVCEERLREREQGRGEDVD 118
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Pred. No. 2.8;
6; Mismatches
                                                                                            on 03-Aug-1995 #text_change 13-Aug-1999
A25812; A05172; A42927
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                              an adhesive glycoprotein with multipl
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C; Function: A; Description: parti
A; Description: parti
C; Superfamily: thron
C; Keywords: beta-hyc
F; 1-18/Domain: signa
F; 19-1170/Product: t
                                                                                                                                                                                                                                                                                                                                                                                    F:378-429/Domain: thrombospondin type I repeat homology <THRIS-
F:434-490/Domain: thrombospondin type I repeat homology <THRIS-
F:491-547/Domain: thrombospondin type I repeat homology <THRIS-
F:491-547/Domain: brombospondin type I repeat homology <THRIS-
F:551-586/Domain: BGF homology <BGFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: the list of in C; Complex: homotrimer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Partial amino acid sequence of human thrombospondin as A;Reference number: A25812; MUID:87157592
A;Accession: A25812
A;Molecule type: mRNA
A;Residues: 1-83, A',85-397 <KOB>
A;Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PIDA:Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PIDA:Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PIDA:Cross-references: GB:M25631; NID:g538353; PIDN:AAA36741.1; PIDA:Cross-reference number: A5172; MUID:86287276
A;Accession: A05172; MUID:86287276
                                                                                                                                                                                                                                                                                    F:551-586/Domain: EGF homology <EGF1>
F:650-689/Domain: EGF homology <EGF>
F:926-928/Region: cell attachment (R-G-D) motif
F:171-232/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 15q15-15q15
A;Introns: 23/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Gene: GDB:THBS1; TSP1; TSP
A:Gross-references: GDB:120438; OMIM:188060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Sun, X.; Skorstengaard, K.; Mosher, D.F. J. Cell Biol. 118, 693-701, 1992
A;Title: Disulfides modulate RGD-inhibitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:M14326; NID:q340005; PIDN:AAA61237.1; PID:q553801 A:Note: parts of this sequence, including the amino end of the mature pr R:Sun, X.; Skorstengaard, K.; Mosher, D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Residues: 1-83,'A',85-522,'A',524-1170 <HEN>
A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
A;Cross-references: EMBL:X14787; NID:g37464; PIDN:CAA32889.1; PID:g37465
A;Note: parts of this sequence, including the amino end of the mature pro
R;Kobayashi, S.; Eden-McCutchan, F.; Framson, P.; Bornstein, P.
Biochemistry 25, 8418-8425, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:J04835
R;Hennessy, S.W.; Frazier, B.A.; Kim, D.D.; Deckwerth, T.L.; Baumgartel, D.M.; Rotw J. Cell Biol. 108, 729-736, 1989
A;Title: Complete thrombospondin mRNA sequence includes potential regulatory sites A;Reference number: A30140; MUID:89139590
A;Accession: A30140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;317-375/Domain: von Willebrand factor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 987-1003 <SUN>
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A:Note: parts of this sequence, including the amino end of the mature protein, were R:Laherty, C.D.; Gierman, T.M.; Dixit, V.M.
J. Biol. Chem. 264, 11227-11227, 1989
A:Tittle: Characterization of the promoter region of the human thrombospondin gene. D A:Reference number: A34274; MUID:89291870
A:Accession: A34274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: Cys-992 is shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A42927; MUID:92348511
A; Accession: A42927
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A; Residues: 1-83, 'A', 85-374, 'RC' <DIX>
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A;Cross-references: GB:
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   Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description: participates in cell migration and adhesion, and in platelet aggregation; Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vor keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; trime;
                                                                                                                                                       270,274/Disulfide bonds: interchain #status predicted 610/Modified site: erythro-beta-hydroxyasparagine (Asn) #status 1051/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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   l Similarity
15; Conser
   Conservative
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                                26.6%;
39.5%;
   6
                                Score
Pred.
Mismatches
                                67;
No.
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                                DB 1;
3.9;
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                                                              Length 1170
   Indels
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   6,
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A;Molecule 1, 170 < LAW>
A;Rosidues: 1-1170 < LAW>
A;Rosidues: 1-1170 < LAW>
A;Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; A;Cross-references: GB:M62469; GB:M62468; GB:M62469; GB:M62470; RBC2465; GB:M62466; GB:M62470; R;Bornstein, P; Alfi, D; Devarayalu, S; Framson, P; Li, P. J. Biol. Chem. 265, 16691-16698, 1990
A;Title: Characterization of the mouse thrombospondin gene and A;Paference number: A37905; MUID:90375546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 19-26, 7%, 28-37 < CHE>
C; Complex: homotrimer, disulfide linked
C; Superfamily: thrombospondin 1; EGF homology; thrombospondin
C; Keywords: calcium binding; glycoprotein; homotrimer
F; 1-18/Domain: signal sequence # status predicted < SIG>
                                                                                                                                                                                                                                                                 F;19-1170/Product: thrombospondin 1 *status predicted <MAT> F;317-375/Domain: von Willebrand factor type C repeat homology F;317-375/Domain: thrombospondin type 1 repeat homology <THR1> F;434-490/Domain: thrombospondin type 1 repeat homology <THR2> F;491-547/Domain: thrombospondin type 1 repeat homology <THR3> F;491-547/Domain: thrombospondin type 1 repeat homology <THR3> F;551-586/Domain: EGF homology <EGF> F;551-86/Domain: EGF homology <EGF> CRGF>
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A;Title: Characterization of mouse thrombospondin 2 sequence and expression during (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change
C:Accession: A40558; A37905; B42587; S68787
C:Accession: A40558; A37905; B42587; Copeland, N.G.; Gilbert,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S68787;
A; Accession: S68787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Title: Expression and initial characterization of recombinant mouse thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Chen, H.; Aeschlimann, D.; FEBS Lett. 387, 36-41, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: mRNA
A;Residues: 1-1152,'P',1154-1170 <LAH>
A;Cross-references: GB:M87276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A42587; MUID:92147683 A;Accession: B42587
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A; Residues: 1-490 <BOR>
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A;Title: Characterization of the murine thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone
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RSCDSLNNRCEGSSVQTRTCHIQECDKRFKQDGGWSHW
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musculus (house mouse)
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                                                                                                                  Score 67; DB Pred. No. 3.9; 6; Mismatches
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NID:g511867; PIDN:AAA5
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protein

Arabidopsis thaliana

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R;Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.S. Cell 82, 89-100, 1995
A;Title: The large diverse gene family var encodes proteins involved in cytoadherence an A;Reference number: Z20487; MUID:95330813
A;Accession: T28432
A; Molecule type: DNA
A; Residues: 1-3078 <
A; Cross-references:
                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                               N;Alternate names: erythrocyte membrane binding protein 1 (EMP1)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: sugar transport
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-524/Product: 62K sucrose-binding protein #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
JQ1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: protein F2K15.210
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T45840
                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
                                                                                                                                                                                                                                                                                                           T28432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L06038; NID:g1431744; PIDN:AAB03894.1; C;Superfamily: glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-524 < GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: JQ1730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Grimes, H.D.; Overvoorde, P.J.; Ripp, K.; Franceschi, V.R.; Hitz, W.D. Plant Cell 4, 1561-1574, 1992
A;Title: A 62-kD sucrose binding protein is expressed and localized in ta;Reference number: JQ1730; MUID:93104680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C;Accession: JQ1730
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A; Introns: 53/2; 98/3;
A; Note: F2K15.210
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A; Residues: 1-554 <RIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62K sucrose-binding protein precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AL132956
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                             34
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                                                                                                                                                                                                                                                                                                                                                                                           EEEDPELVTCKHQCQQQQQYTEGDKRVCLQSCDR
                    1-3078 <SUX>
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  EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA75396.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB;
Pred. No. 5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              localized in tissues actively
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                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
    1088
                                          22 GOMRRCVSQCDKRFEEDIDWSKYD 45
GEKRRCLSTTDVTELAEIDWDKID 1111
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hypothetical protein F6H11.110 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 09-Apr.1999 #sequence_revision 09-Apr.1999 #text_change 13-Aug-1999 C;Accession: T05892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid F31A3.
A;Reference number: 220667
A;Accession: T29699
                                                                                                                      A; Map position: 5
A; Introns: 72/3;
                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-1421 <BEV>
A; Cross-references: EMBL: ALO21684
                                                                                                                                                                                                                                                                                                  R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: X
A;Introns: 18/3; 160/3
C;Superfamily: ultra-high-sulfur keratin
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Best Local Similarity
"~+~hes 13; Conserv
                                                                                                      A; Note: F6H11.110
                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                 A; Experimental source: cultivar Columbia;
                                                                                                                                                                                                                                                             A; Reference number: Z15456
A; Accession: T05892
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A; Residues: 1-242 <MUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F31A3.1 - Caenorhabditis elegans
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                                        Query Match
                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AQCEPQCQQSCQQQCVQQQQS--MQQCASACTK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 33.3 les 11; Conservative
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                                                                                                                        142/3; 227/2;
      Conservative
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                      23.0%;
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                                                                                                                        344/3;
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      Ψ
                      Score 58;
Pred. No.
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Pred. No. 70;
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      Mismatches
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                                                                                                                      372/3; 941/2;
                                                                                                                                                                                 BAC clone F6H11
                        53;
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                                                                                                                      1016/3; 1038/3; 1055/1;
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                                          Length 1421;
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    Indels
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Gaps
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                                                                                                                      1095/2;
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A-type inclusion protein - vaccinia virus (strain WR)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 29-Oct-1999
C;Accession: A41701; A40825; S29908
R;De Carlos, A; Paez, E.
Virology 185, 768-778, 1991
A;Title: Isolation and characterization of mutants of vaccinia virus with a modified 94-A;Reference number: A41701; MUID:92074241
A;Accession: A41701
A;Molecule type: DNA
A;Residues: 1-725 <DEC>
A;Cross-references: GB:M76371; NID:g335683; PIDN:AAA48275.1; PID:g335684
R;Amegadzie, B:Y; Sisler, J.R.; Moss, B.
Virology 186, 777-782, 1992
A;Title: Frame-shift mutations within the vaccinia virus A-type inclusion protein gene.
A;Accession: A40825; MUID:92124754
                                                                                                                                                                                                                              A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-586,'KQ',589-609,'R',611-618,620-682,'S',684-725 <AM2>
A;Cross-references: EMBL:X57318; NID:g62239; PIDN:CAA40574.1; PID:g62241
C;Superfamily: cowpox virus A type inclusion protein
C;Keywords: inclusion protein
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A;Residues: 1-586,'KQ',589-609,'R',611-618;620-682,'S',684-725 <AME>
A;Cross-references: GB:M61187; NID:g335782; PIDN:AAA48321.1; PID:g335784
R;Amegadzie, B.Y.
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R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.; Salzborg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rifin PFB1005w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
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A;Experimental source: clone 3D7
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A; Residues: 1-316 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A;Reference number: A71600; MUID:99021743 A;Accession: G71600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
G71600
rifin PFB1005w -
                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 15; Conserv
                              12 KRQCMQLETSGQMRRCVSQCDKRFEEDIDWSK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 FDRQTSERFEEYDE-----RMKDKRRKCKEQCDKDIQEII 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 FDRQ-----EYEECKRQCMQLETSGQMRRCVSQCDKRFEEDI 39
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%;
                                                                                                                  22.6%; Score 57; DB 1; Length 725; 40.6%; Pred. No. 38;
                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57; DB 2; Length 316; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                      6,
                                                                                      Indels
                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                   Gaps
                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ε.V.;
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Db 550 KRRNVEWELS-RLRRDIKECDK-YKEDLDKAK 579

Search completed: March 1, 2001, 15:52:28 Job time: 552 sec

